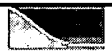
Basic UniProtKB Entry Viewer

Protein Q847D1_NODSP  New Query | Submit Annotation | Download Protein | Bookmark Protein

Basic | **Extended** Viewers: Fasta | Flat File | XML | ExPASy | SRS | PIR

General information about the UniProt/TrEMBL entry	
Entry name	**Q847D1_NODSP**
Primary accession number	**Q847D1**
Entered in TrEMBL	Release 24, 01-JUN-2003
Sequence was last modified	Release 24, 01-JUN-2003
Annotations were last modified	Release 26, 01-MAR-2004
Protein description	
Protein name	**Putative beta-carotene ketolase**
Origin of the protein	
From	Nodularia spumigena[TaxID:70799]
Taxonomy	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nodularia.
References	
[1]	NUCLEOTIDE SEQUENCE. STRAIN=NSOR10; DOI=10.1007/s00239-002-2415-0; MEDLINE=22549861; PubMed=12664164; [NCBI, ExPASy, EBI, Israel, Japan] Moffitt M.C., Neilan B.A.; "Evolutionary affiliations within the superfamily of ketosynthases reflect complex pathway associations."; J. Mol. Evol. 56:446-457(2003).
[2]	NUCLEOTIDE SEQUENCE.

	STRAIN=NSOR10; DOI=10.1128/AEM.70.11.6353-6362.2004; PubMed=15528492; [NCBI, ExPASy, EBI, Israel, Japan] Moffitt M.C., Neilan B.A.; "Characterization of the nodularin synthetase gene cluster and proposed theory of the evolution of cyanobacterial hepatotoxins."; Appl. Environ. Microbiol. 70:6353-6362(2004).
Cross-references	
EMBL	AY210783; AAO64399.1; -; Genomic_DNA.[EMBL/ GenBank/ DDBJ] [CoDingSequence]
GO	Cellular component — membrane — GO:0016020 — inferred from electronic annotation Molecular function — oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water — GO:0016717 — inferred from electronic annotation Molecular function — oxidoreductase activity, acting on single donors with incorporation of molecular oxygen — GO:0016701 — inferred from electronic annotation Biological process — carotene metabolism — GO:0016119 — inferred from electronic annotation Biological process — fatty acid desaturation — GO:0006636 — inferred from electronic annotation [QuickGO]
InterPro	IPR011393; Carotene_ketolas. IPR005804; Fa_desat. IPR010257; FA_desat_sub. Graphical view of the domain structure
Pfam	PF00487; FA_desaturase; 1. Pfam graphical view of domain structure
PIRSF	PIRSF027840; Carotene_ketolas; 1.
ProDom	PD001081; FA_desat_sub; 1. [Domain structure/ List of seq. sharing at least 1 domain]
Sequence information	
Length	229 AA
Molecular weight	27832 Da

CRC64	71C9271BB371C95B [This is a checksum on the sequence]

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MAIAIISIWA ISLGLLLYID ISQFKFWMLL PLIFWQTFLY TGLFITAHDA  50

MHGVVFPKNP KINHFIGSLC LFLYGLLPYQ KLLKKHWLHH HNPASETDPD 100

FHNGKQKNFF AWYLYFMKRY WSWLQIITLM IIYNLLKYIW HFPEDNMTYF 150

WVVPSILSSL QLFYFGTFLP HSEPVEGYKE PHRSQTISRP IWWSFITCYH 200

FGYHYEHHEY PHVPWWQLPE IYKMSKSNL                        229
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Pop-Up Fasta View **UniParc | UniRef100 | UniRef90 | UniRef50**